

FIG. 1A

		(SEQ ID NO:1)																				(SEQ ID NO:2)																			
		GAG	ACT	CAC	GGT	CAA	GCT	AAG	GCG	AAG	AGT	GGG	TGG	CTG	AAG	CCA	TAC	TAT	TTT	ATA	GAA	GAG	ACT	CAC	GGT	CAA	GCT	AAG	GCG	AAG	AGT	GGG	TGG	CTG	AAG	CCA	TAC	TAT	TTT	ATA	GAA
		↓																				↓																			
		M																				E																			
61	TTA	ATG	GAA	AGC	AGA	AAA	GAC	ATC	ACA	AAC	CAA	GAA	GAA	CTT	TGG	AAA	ATG	AAG	CCT	AGG	TTA	ATG	GAA	AGC	AGA	AAA	GAC	ATC	ACA	AAC	CAA	GAA	GAA	CTT	TGG	AAA	ATG	AAG	CCT	AGG	
121	R	AN	L	E	E	D	D	Y	L	H	K	D	T	G	E	T	S	M	L	K	R	AN	L	E	E	D	D	Y	L	H	K	D	T	G	E	T	S	M	L	K	
181	AGA	AAT	TTA	GAA	GAA	GAC	GAT	TAT	TG	CAT	AAG	CAC	ACG	GGA	GAG	ACC	AGC	ATG	CTA	AAA	AGA	AAT	TTA	GAA	GAA	GAC	GAT	TAT	TG	CAT	AAG	CAC	ACG	GGA	GAG	ACC	AGC	ATG	CTA	AAA	
241	R	P	V	L	L	H	L	H	Q	T	A	H	A	D	E	F	D	C	P	S	R	P	V	L	L	H	L	H	Q	T	A	H	A	D	E	F	D	C	P	S	
301	AGA	CCT	GTG	CTT	TTG	CAT	TTG	CAC	CAA	ACC	GCC	CAT	GCT	GAT	GAA	TTT	GAC	TGC	CCT	TCA	AGA	CCT	GTG	CTT	TTG	CAT	TTG	CAC	CAA	ACC	GCC	CAT	GCT	GAT	GAA	TTT	GAC	TGC	CCT	TCA	
361	E	L	Q	H	T	Q	E	L	F	P	Q	W	H	L	P	I	K	I	A	A	E	L	Q	H	T	Q	E	L	F	P	Q	W	H	L	P	I	K	I	A	A	
421	GAA	CTT	CAG	CAC	ACA	CAG	GAA	CTC	TTT	CCA	CAG	TGG	CAC	TTG	CCA	ATT	AAA	ATA	GCT	GCT	GAA	CTT	CAG	CAC	ACA	CAG	GAA	CTC	TTT	CCA	CAG	TGG	CAC	TTG	CCA	ATT	AAA	ATA	GCT	GCT	
481	I	I	A	S	L	T	F	L	Y	T	L	R	E	V	I	H	P	L	A	A	I	I	A	S	L	T	F	L	Y	T	L	R	E	V	I	H	P	L	A	A	
541	ATT	ATA	GCA	TCT	CTG	ACT	TTT	CTT	TAC	ACT	CTT	CTG	AGG	GAA	GTA	ATT	CAC	CCT	TTA	GCA	ATT	ATA	GCA	TCT	CTG	ACT	TTT	CTT	TAC	ACT	CTT	CTG	AGG	GAA	GTA	ATT	CAC	CCT	TTA	GCA	
601	T	S	H	Q	Q	Y	F	Y	K	I	P	I	L	V	I	N	K	V	L	P	T	S	H	Q	Q	Y	F	Y	K	I	P	I	L	V	I	N	K	V	L	P	
661	ACT	TCC	CAT	CAA	CAA	TAT	TTT	TAT	AAA	ATT	CCA	ATC	CTG	GTC	ATC	AAC	AAA	GTC	TTG	CCA	ACT	TCC	CAT	CAA	CAA	TAT	TTT	TAT	AAA	ATT	CCA	ATC	CTG	GTC	ATC	AAC	AAA	GTC	TTG	CCA	
721	M	V	S	I	T	L	L	A	L	V	Y	L	P	C	G	V	I	A	I	V	M	V	S	I	T	L	L	A	L	V	Y	L	P	C	G	V	I	A	I	V	
781	ATG	GTT	TCC	ATC	ATC	CTC	TTG	GCA	TTG	GTT	TAC	CTG	CAC	GGT	GTG	ATA	GCA	GCA	ATT	GTC	ATG	GTT	TCC	ATC	ATC	CTC	TTG	GCA	TTG	GTT	TAC	CTG	CAC	GGT	GTG	ATA	GCA	GCA	ATT	GTC	
841	Q	L	H	N	G	T	K	Y	K	K	F	P	H	W	L	D	K	W	M	L	Q	L	H	N	G	T	K	Y	K	K	F	P	H	W	L	D	K	W	M	L	
901	CAA	CTT	CAT	AAT	GGA	ACC	AAG	TAT	AAG	AAG	TTT	CCA	CAT	TGG	TTG	GAT	AAG	TGG	ATT	TGA	CAA	CTT	CAT	AAT	GGA	ACC	AAG	TAT	AAG	AAG	TTT	CCA	CAT	TGG	TTG	GAT	AAG	TGG			

FIG. 1B

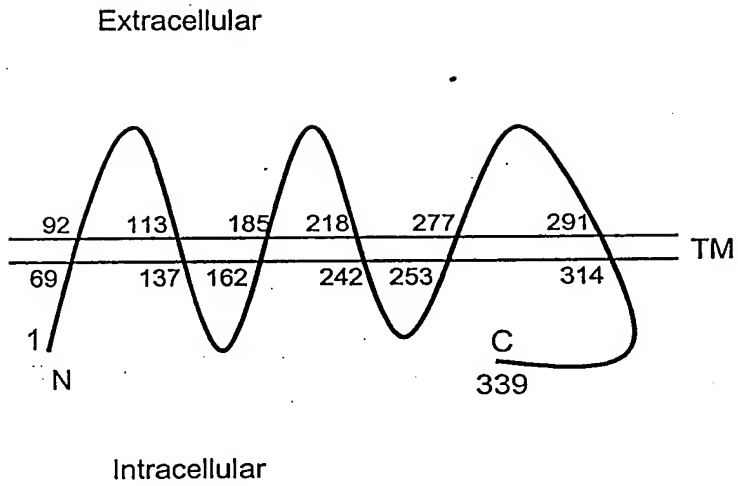
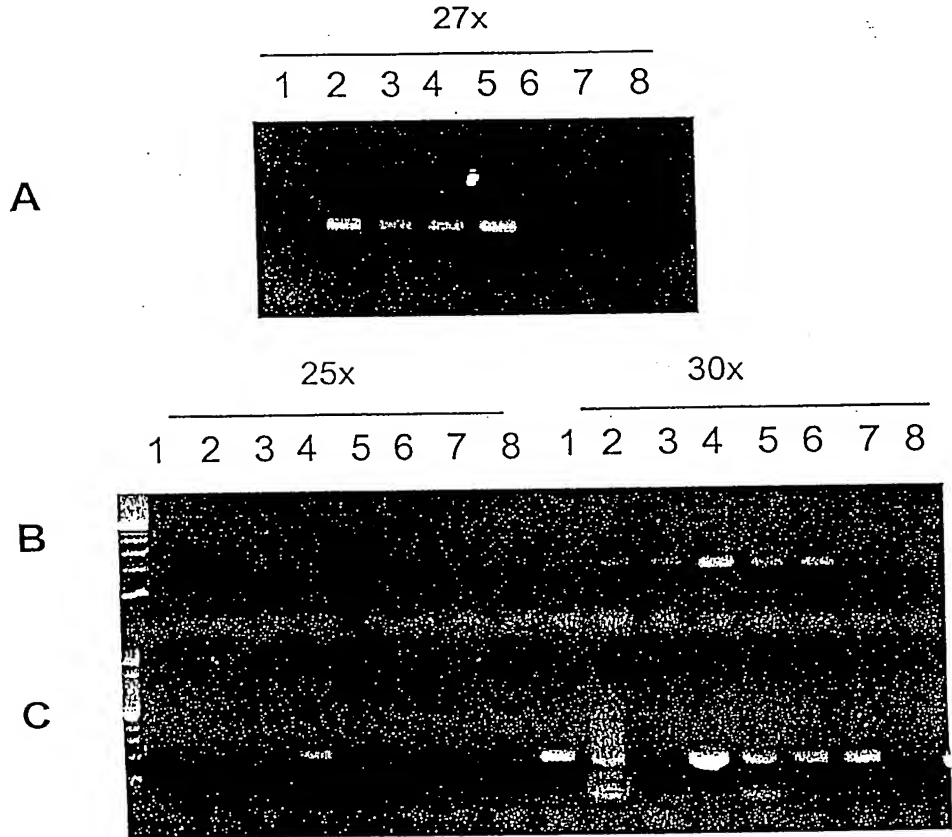


FIG. 1C

5' GGC GGA GGC GGA GGC GGA GGG CGA GGG GCG GGG AGC GCC GCC TGG AGC GCG
GCA GGT CAT ATT GAA CAT TCC AGA TAC CTA TCA TTA CTC GAT GCT GTT GAT
AAC AGC AAG 3' (SEQ ID NO:3)

FIG. 2



Panels:

A

1. Brain
2. Prostate
3. LAPC-4 AD
4. LAPC-4 AI
5. LAPC-9 AD
6. HeLa
7. Murine cDNA
8. Neg. control

B

1. Brain
2. Heart
3. Kidney
4. Liver
5. Lung
6. Pancreas
7. Placenta
8. Skeletal Muscle

C

1. Colon
2. Ovary
3. Leukocytes
4. Prostate
5. Small Intestine
6. Spleen
7. Testis
8. Thymus

FIG. 3A

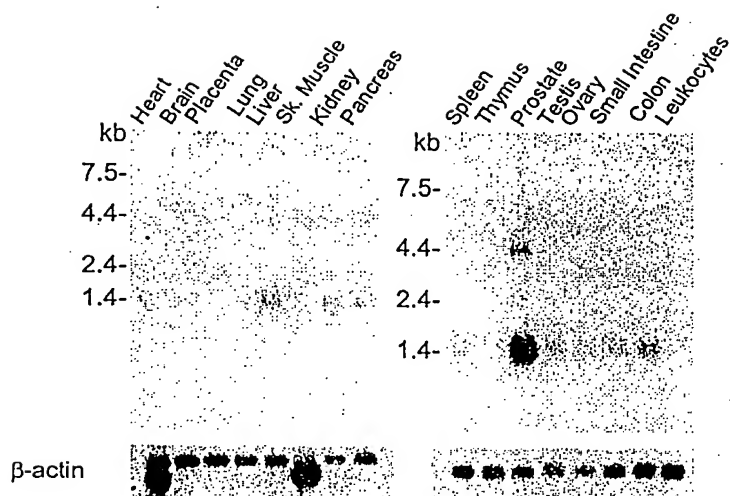


FIG. 3B

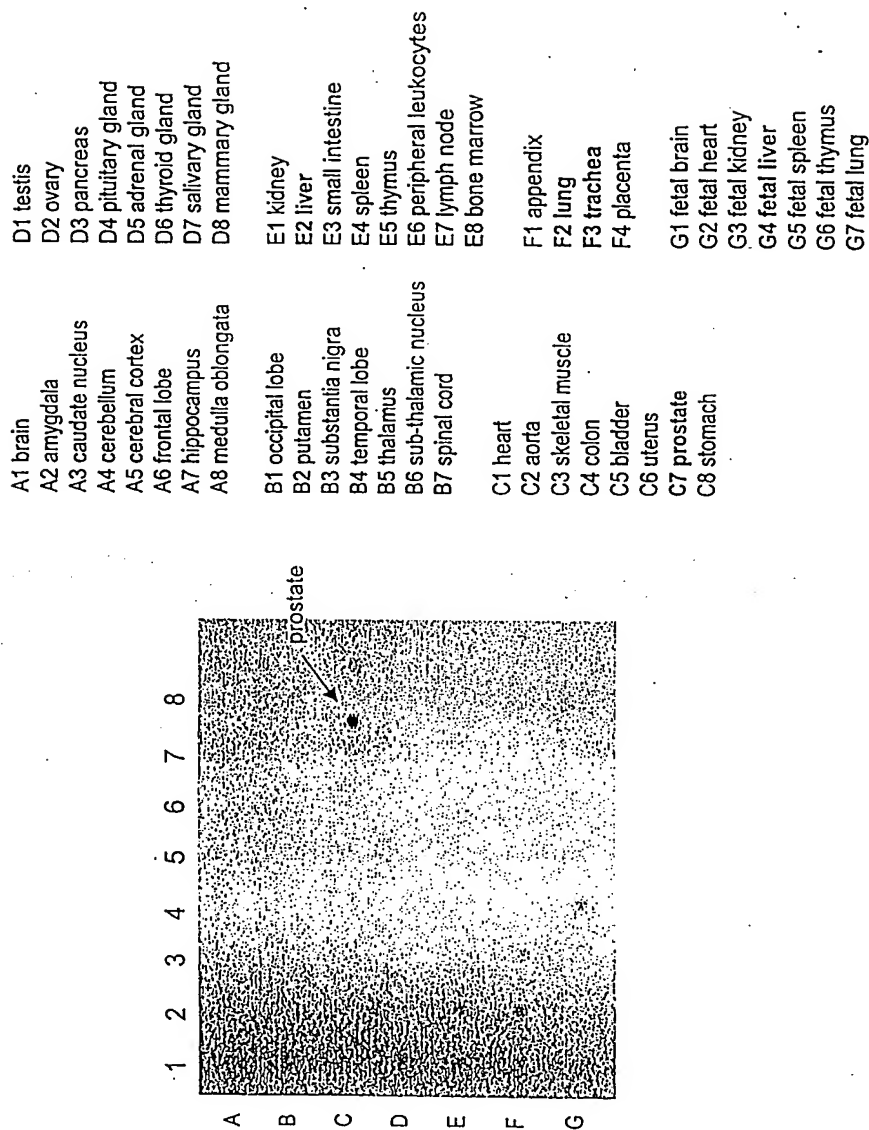


FIG. 4-1

GGGGCCCGCACCTCTGGGCAGCAGCGGCAGCCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCC
ATACTATTTTATAGAATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGG
AGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGACCTGTGCTTTTGC
ATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAACTTCAGCACACACAGGAACCTTTCCACA
GTGGCACTTGCCAAATTAATAGCTGCTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAAT
CACCCCTTAGCAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATGG
TTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAACCTTCATAATGAACCAA
GTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTT
GCTGTACTGCATGCAATTTATAGTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCAT
ATCAACAGGTCCAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTGGAGAATTGGAGATTTATGTGCTCT
GGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCTGTGAGTGACTCTTTGACATGG
AGAGAATTTCACTATATTCAGGTAATAATATATAAAATAACCTAAGAGGTAATCTTCTTTTTGTGTTTATGAT
ATAGAATATGTTGACTTTACCCATAAAAAATAACAAATGTTTTTCAACAGCAAAGATCTTATACTGTGCCAATT
AATAATGTGCTCTCCTGTTGTTTTCCCTATTGCTTCTAATTAGGACAAGTGTTCTTAGACATAAATAAAGGCAT
TAAATATTCTTTGTTTTTTTTTTTTGTTTGTGTTTTTGTGTTGTTGTTTTTGTGATGAAGTCTCG
CTCTGTTGCCCATGCTGGAGTACAGTGGCAGCATCTCGGCTCACTGCAACCTGCGCCTCCTGGGTTGAGCGATT
TCTTGCTCAGCCTCCTGAGTAGCTGGGATTACAGGCACCCATCACCATGTCCAGCTAATTTTTGTATTTTAGTA
GAGACAGGGTTTTCCCATGTTGGCCAGGCTGGTCTCGATCTCCTGACCTCAAATGATCCGCCACCTCGGCCTCCC
AAAGTGCTGGGATGACAGTTGTGAGGCCACCACTCAGCCTGCTCTTTCTAATATTTGAAACTTGTAGACAATTT
GCTACCATCTAATGTGATATTTAGGAATCCAATATGCATGGTTTATTATTTCTTAAAAAAATATTCTTTTACC
TGTCACCTGAATTTAGTAATGCCTTTTATGTTACACAACCTAGCACTTTCAGAAACAAAACCTCTCCTTGAAA
TAATAGAGTTTTATCTACCAAAGATATGCTAGTGTCTCATTTCAAAGGCTGCTTTTTCCAGCTTACATTTATAT
ACTTACTCACTTGAAGTTTCTAAATATTCTTGTAATTTTAAACTATCTCAGATTTACTGAGGTTTATCTTCTGGT
GGTAGATTATCCATAAGAAGAGTGATGTGCCAGAATCACTCTGGGATCCTTGCTGACAAGATTCAAAGGACTAAA

FIG. 4-2

TTTAATTCAGTCATGAACACTGCCAATTACCGTTTATGGGTAGACATCTTTGGAAATTTCCACAAGGTCAGACATT
CGCAACTATCCCTTCTACATGTCCACACGTATACTCCAACACTTTATTAGGCATCTGATTAGTTTGAAAGTATGC
CTCCATCTGAATTAGTCCAGTGTGGCTTAGAGTTGGTACAACATTCTCACAGAATTTCTTAATTTTGTAGGTTACG
CCTGATAACCACTGGAGTTCTTTGGTCTCATTAAATAGCTTTCTTCACACATTGCTCTGCCTGTTACACATATGA
TGAACACTGCTTTTTAGACTTCATTAGGAATTTAGGACTGCATCTTGACAACCTGAGCCTATTCTACTATATGTACA
ATACCTAGCCATAATAGGTATACAATACACATTTGGTAAACTAATTTCAACCAATGACATGTATTTTCAACT
AGTAACCTAGAAATGTTTCACTTAAAACTGAGAAGTGGTTACACTACAAGTTACCTGGAGATTCATATATGAAA
ACGCAAACTAGCTATTTGATTGTATTCACTGGGACTTAAGAATGCGCCTGAATAATGTGAGTTCGATTTGTTCT
GGCAGGCTAATGACCATTTCCAGTAAAGTGAATAGAGGTCAGAAGTCGTATAAAAGAGGTGTTGTCAGAACCCGT
TGAGATTACATAGGTGAACAACTATTTTAAAGCAACTTTATTGTGTAGTGACAAAGCATCCCAATGCAGGCTGAA
ATGTTTCATCACATCTCTGGATCTCTCTATTTTGTGCAGACATTGAAAAAATTGTTTCATATTATTTCCATGTTATC
AGAATATTTGATTTTTTAAAAACATAGGCCAAGTTCATTCACTTCATTATTCATTTATCAAAATCAGAGTGAATCA
CATTAGTCGCCTTCACAACTGATAAAGATCACTGAAGTCAAATTGATTTTTGCTATAATCTTCAATCTACCTATAT
TTAATTGAGAATCTAAATGTACAAATCATTGTGTTGATTCTGCAGTGATCCTGTATATAAGTAAAGACTCAGTCCCT
GATTTTAGGTATCCTGTGAAAAGCAGAATTAAGACAAATACACAAGAGACAAAGCACAAAAAATAAATATCATAAG
GGGATGAACAAAATGGTGGAGAAAGAGTAGACMAAGTTTTTGATCACCTGCCTTCAAGAAAGGCTGTGAATTTTG
TTCCTTAGACAGCTTGAGACAAGAAATTACCCAAAAGTAAGGTGAGGAGGATAGGCAAAAAGAGCAGAAAGATG
TGAATGGACATTGTTGAGAAATGTGATAGGAAAACAATCATAGATAAAGGATTTCCAAGCAACAGAGCATATCCAG
ATGAGGTAGGATGGGATAAATCTTATTGAACCAATCTCACCAATTTTGTTCCTTTTGCAGAGCAAGCTAGGA
ATTGTTTCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGATATAAAACAATTG
TATGGTATACACCTCCAATTTTATGATAGCTGTTTTCTTCCAATTGTTGTCTGATATTTAAAGCATACTATT
CCTGCCATGCTTGAGGAAGAAGATACTGAAGATTAGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACCTGAG
ATATGTTCCAGTTGTAGAAATTAAGTGTACACACATTTTGTTCATATTGATATATTTTATCACCACATTTTCA
AGTTTGTATTTGTTAATAAAATGATTATCAAGGAAAAAAAAAAAAAAAAAAAAA (SEQ ID NO:6)

FIG. 5

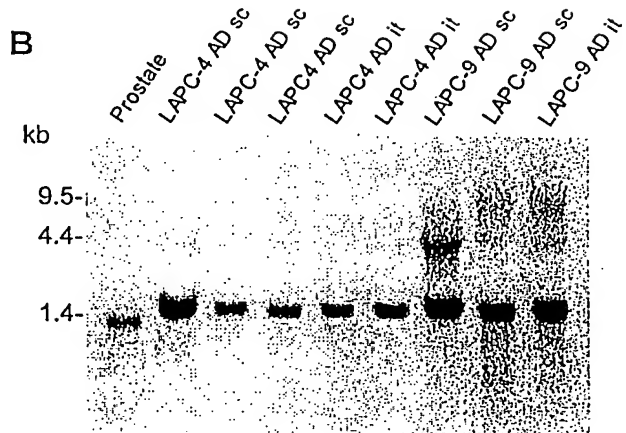
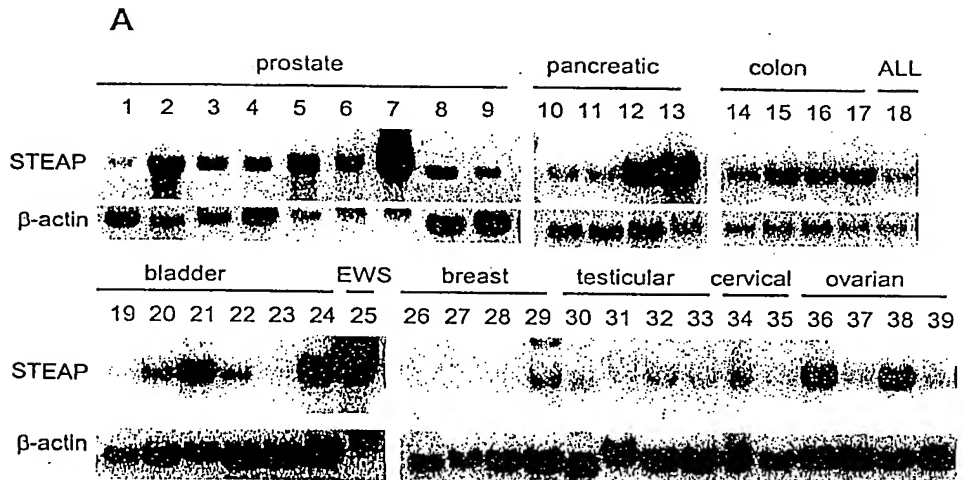
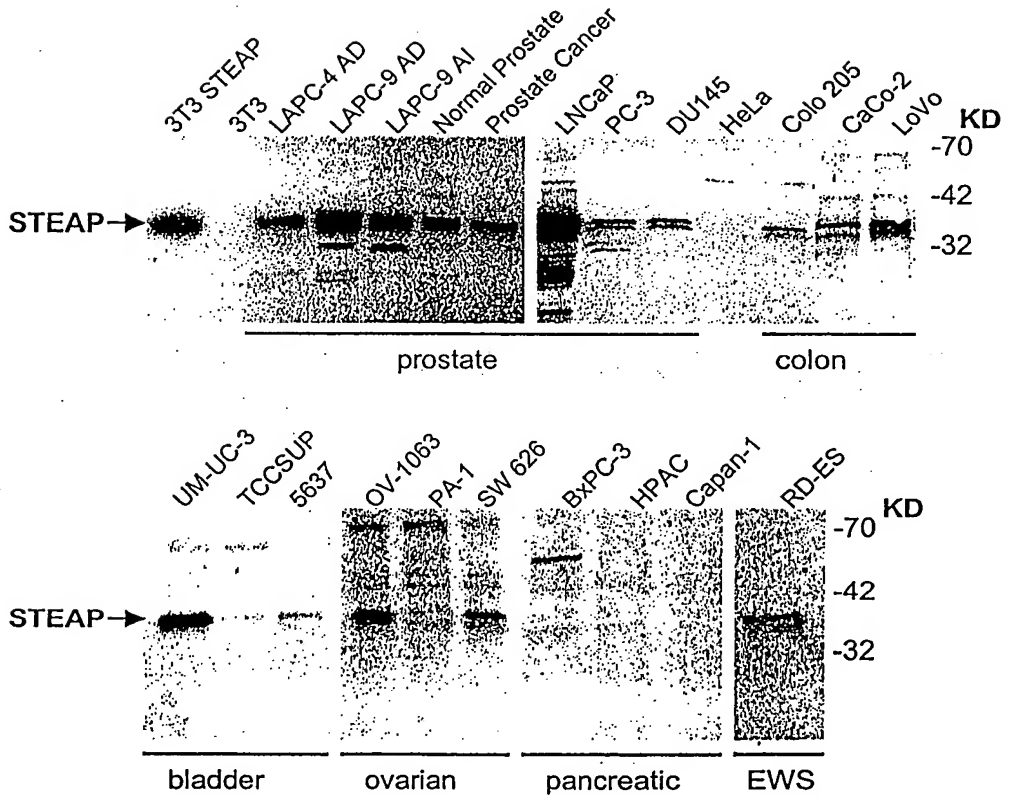


FIG. 6



9.99

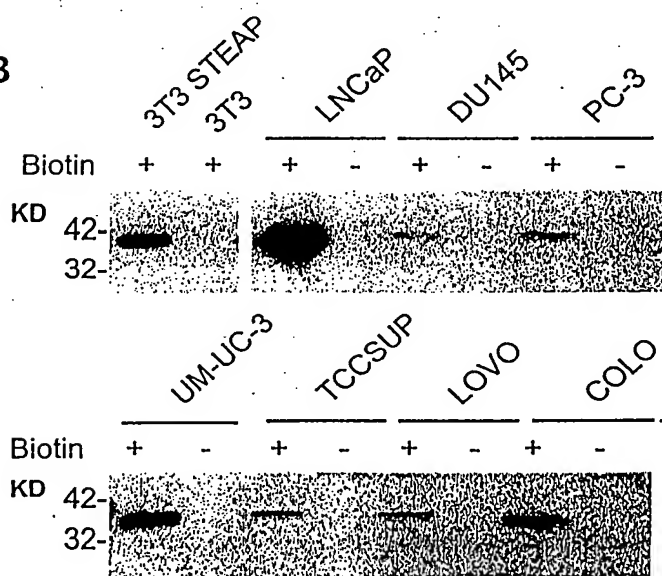
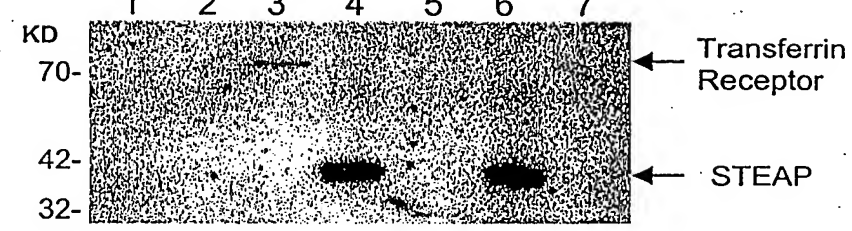


FIG. 9

		10		19		28		37		46		55						
5'	GAC	TTT	TAC	AAA	ATT	CCT	ATA	GAG	ATT	GTG	AAT	AAA	ACC	TTA	CCT	ATA	GTT	GCC
	Asp	Phe	Tyr	Lys	Ile	Pro	Ile	Glu	Ile	Val	Asn	Lys	Thr	Leu	Pro	Ile	Val	Ala
		64			73			82		91		100						109
	ATT	ACT	TTG	CTC	TCC	CTA	GTA	TAC	CTC	GCA	GGT	CTT	CTG	GCA	GCT	GCT	TAT	CAA
	Ile	Thr	Leu	Leu	Ser	Leu	Val	Tyr	Leu	Ala	Gly	Leu	Leu	Ala	Ala	Ala	Tyr	Gln
		118			127			136		145		154						163
	CTT	TAT	TAC	GGC	ACC	AAG	TAT	AGG	AGA	TTT	CCA	CCT	TGG	TTG	GAA	ACC	TGG	TTA
	Leu	Tyr	Tyr	Gly	Thr	Lys	Tyr	Arg	Arg	Phe	Pro	Pro	Trp	Leu	Glu	Thr	Trp	Leu
		172			181			190		199		208						217
	CAG	TGT	AGA	AAA	CAG	CTT	GGA	TTA	CTA	AGT	TTT	TTC	TTC	GCT	ATG	GTC	CAT	GTT
	Gln	Cys	Arg	Lys	Gln	Leu	Gly	Leu	Leu	Ser	Phe	Phe	Phe	Ala	Met	Val	His	Val
		226			235			244		253		262						271
	GCC	TAC	AGC	CTC	TGC	TTA	CCG	ATG	AGA	AGG	TCA	GAG	AGA	TAT	TTG	TTT	CTC	AAC
	Ala	Tyr	Ser	Leu	Cys	Leu	Pro	Met	Arg	Arg	Ser	Glu	Arg	Tyr	Leu	Phe	Leu	Asn
		280			289			298		307		316						325
	ATG	GCT	TAT	CAG	CAG	GTT	CAT	GCA	AAT	ATT	GAA	AAC	TCT	TGG	AAT	GAG	GAA	GAA
	Met	Ala	Tyr	Gln	Gln	Val	His	Ala	Asn	Ile	Glu	Asn	Ser	Trp	Asn	Glu	Glu	Glu
		334			343			352		361		370						379
	GTT	TGG	AGA	ATT	GAA	ATG	TAT	ATC	TCC	TTT	GGC	ATA	ATG	AGC	CTT	GGC	TTA	CTT
	Val	Trp	Arg	Ile	Glu	Met	Tyr	Ile	Ser	Phe	Gly	Ile	Met	Ser	Leu	Gly	Leu	Leu
		388			397			406		415		424						433
	TCC	CTC	CTG	GCA	GTC	ACT	TCT	ATC	CCT	TCA	GTG	AGC	AAT	GCT	TTA	AAC	TGG	AGA
	Ser	Leu	Leu	Ala	Val	Thr	Ser	Ile	Pro	Ser	Val	Ser	Asn	Ala	Leu	Asn	Trp	Arg
		442			451			460		469		478						487
	GAA	TTC	AGT	TTT	ATT	CAG	TCT	ACA	CTT	GGA	TAT	GTC	GCT	CTG	CTC	ATA	AGT	ACT
	Glu	Phe	Ser	Phe	Ile	Gln	Ser	Thr	Leu	Gly	Tyr	Val	Ala	Leu	Leu	Ile	Ser	Thr
		496			505			514										
	TTC	CAT	GTT	TTA	ATT	TAT	GGA	TGG	AAA	CGA	GCT	3'	(SEQ ID NO:7)					
	Phe	His	Val	Leu	Ile	Tyr	Gly	Trp	Lys	Arg	Ala	(SEQ ID NO:8)						

FIG. 10

STEAP-2, AA508880 (NCI_CGAP Pr6)

ggctcgacttttcttattcctttgtcagagatctgattcatccatatgctagaaaccaacagagtgacttttaca
aaattcctatagagattgtgaataaaaccttacctatagttgccattactttgtctctccctagtataccttgcagg
tcttctggcagctgcttatcaactttattacggcaccaagtataggagatttccaccttgggtggaaacctgggtta
cagtgtagaaaacagcttggattactaagtgtttcttctcgtatggtccatggttgcctacagcctctgctaccga
tgagaaggtcagagagat (SEQ ID NO:9)

STEAP-2, 98P4B6 SSH fragment

TTTGACGCTTTGCAGATACCCAGACTGAGCTGGAACCTGGAATTGTCTTCCTATTGACTCTACTTCTTTAAAGCG
GCTGCCCATTAATTCTCAGCTGTCTTGCACTTAGGTGTACATGTGACTGAGTGTGGCCAGTGAGATGAAGTC
TCCTCAAAGGAAGGCAGCATGTGTCCTTTT (SEQ ID NO:10)

A1139607 (testis EST)

aagaaggagaatccatttagcacctcctcagcctggctcagtgattcatatgtggctttgggaataacttgggtttt
ttctgtttgtactcttgggaatcacttcttggcatctgttagcaatgcagtcactggagagagttccgatttgt
ccagtcctaaactgggttatttgacctgatcttgtgtacagcccacacctgggtgtacggtgggaagagattcctc
agcccttcaaatctcagatgggtatcttctcgcagcctacgtgttagggcttatcattccttgcactgtgctgtga
tcaagtttgtcctaatcatgcatggtgtagacaacaccttacaaggatccgccagggctgggaaaggaaactcaaa
acactagaaaaagcattgaattggaataatcaatatttaaaacaaagttcaatttagctggaaaaaa (SEQ ID NO:11)

R80991 (placental EST)

ggccgcggcancgcctacgacctgggtcaacctggcagtcgaagcaggtcttggccanacaagagccacctctgggtg
aaggaggaggtctggcggaatggagatctacctctccctgggagtgctggccctcgggcaggttgcctctgctggccg
tgacctcactgccgtccattgcaaaactcgcctcaactggagggaagtcagcttcgttcagtcctcactgggcttgt
ggcctcgtgctgagcacactncacacgctcacctacggctggaccccgccctcgaggagagccgctacaagttc
tacctnctccaccttcacgntcacgctgctgggtgccctgcgttcgttcactctgggcaaaagccctgtttntac
tgccttgcatcagccgnaga (SEQ ID NO:12)

(continued)

(Portion of SEQ ID NO:8)

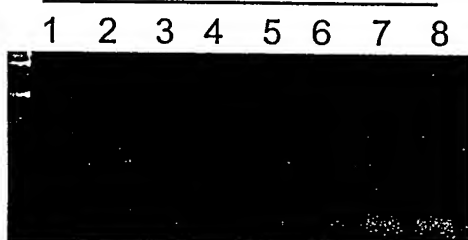
FIG. 11B

	15 16	30 31	45 46	60 61	75 76	90
STEAP-1	MESRDIITNOEELAK	DKPRNLEEDDYLEK	DTGETSMXKGPVLLH	LHQTAADEFDCPSE	LQHTQELFPQWHLFY	KIAAIIASLFLYTL
STEAP-2	-----	-----	-----	-----	-----	-----
STEAP-3	-----	-----	-----	-----	-----	-----
STEAP-4	-----	-----	-----	-----	-----	-----
	105 106	120 121	135 136	150 151	165 166	180
STEAP-1	LREVIHPLATSEQQY	FYKIPILVINKVLP	VSITLLALVLP	GVYLAIVQLANGTKYKIF	PMLEKKNMLTRKQK	ELSPFFAVLHAYSL
STEAP-2	-----	-----	-----	-----	-----	-----
STEAP-3	-----	-----	-----	-----	-----	-----
STEAP-4	-----	-----	-----	-----	-----	-----
	195 196	210 211	225 226	240 241	255 256	270
STEAP-1	SYPMERSRYKLEAW	AYOOQONKEDAWIE	HDVMEIYVSLGIV	GLAIALAVTSIPS	VSDSLTREFEVIOS	VLGTVSLLCTHAI
STEAP-2	-----	-----	-----	-----	-----	-----
STEAP-3	-----	-----	-----	-----	-----	-----
STEAP-4	-----	-----	-----	-----	-----	-----
	285 286	300 301	315 316	330 331	345 346	360
STEAP-1	IFAMKNWIDIKQFVN	YTPPTFMIAVLPV	VLLPKSILPFCIRK	KIKIRHGMEDVTKI	NKTEICSQL	339 (SEQ ID NO:2)
STEAP-2	-----	-----	-----	-----	-----	-----
STEAP-3	-----	-----	-----	-----	-----	-----
STEAP-4	-----	-----	-----	-----	-----	-----

100019277 0040F00N

FIG. 14A

26x



1. Brain
2. Prostate
3. LAPC-4 AD
4. LAPC-4 AI
5. LAPC-9 AD
6. HeLa
7. Murine cDNA
8. Neg control

FIG. 14B

1 2 3 4 5 6 7 8

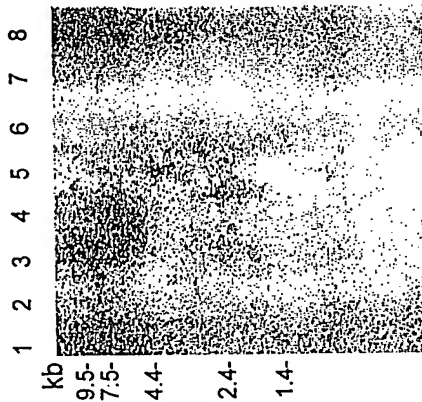
25x

30x



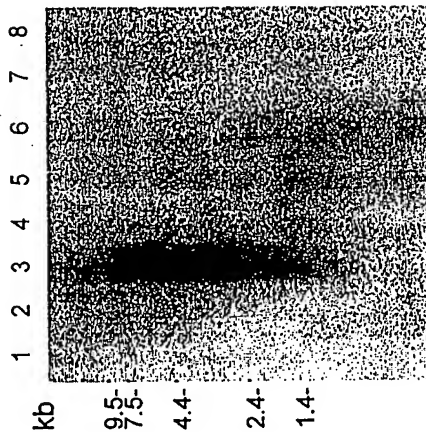
1. Colon
2. Ovary
3. Leukocytes
4. Prostate
5. Small Intestine
6. Spleen
7. Testis
8. Thymus

FIG. 15A



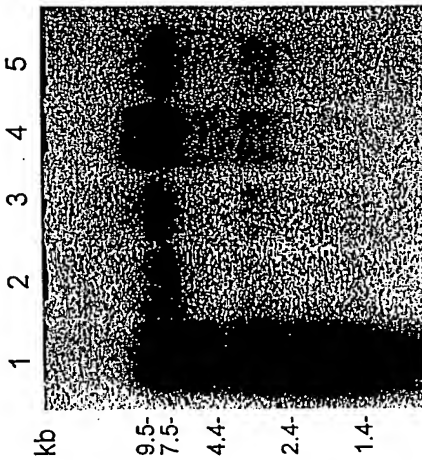
1. Heart
2. Brain
3. Placenta
4. Lung
5. Liver
6. Skeletal Muscle
7. Kidney
8. Pancreas

FIG. 15B



1. Spleen
2. Thymus
3. Prostate
4. Testis
5. Ovary
6. Small Intestine
7. Colon
8. Leukocytes

FIG. 15C



1. Prostate
2. LAPC-4 AD
3. LAPC-4 AI
4. LAPC-9 AD
5. LAPC-9 AI

FIG. 16

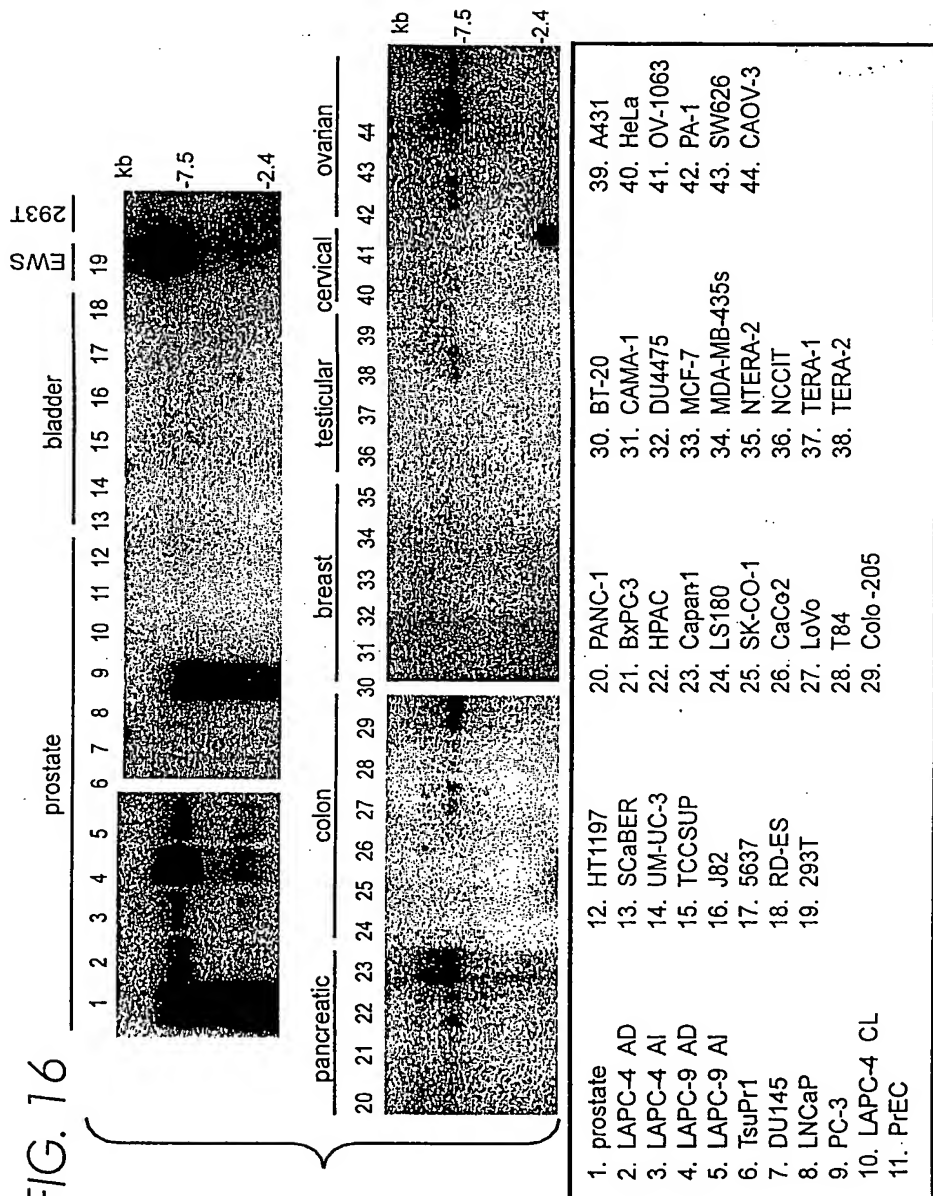


FIG. 17

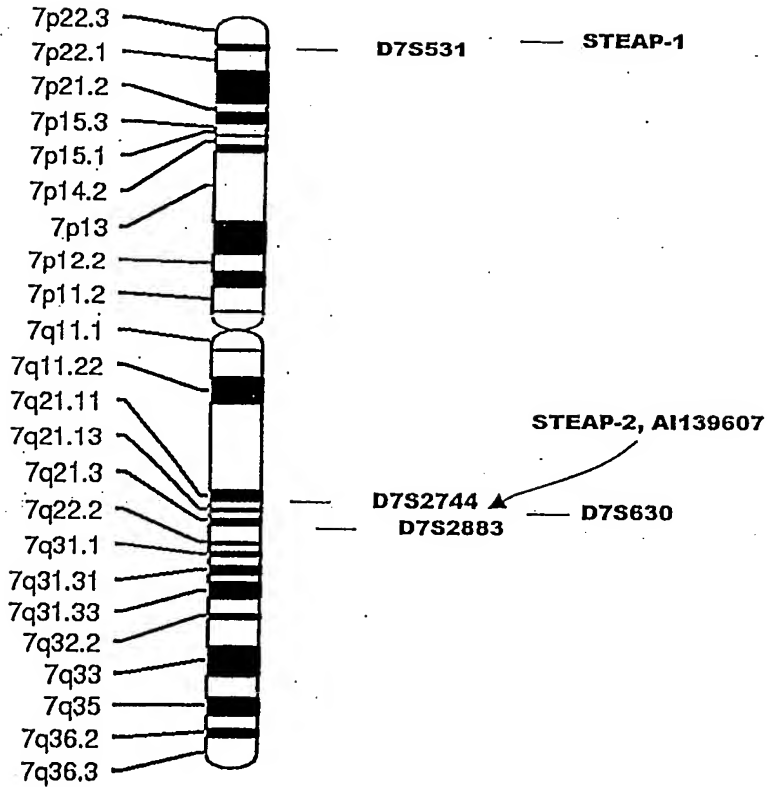


FIG. 19

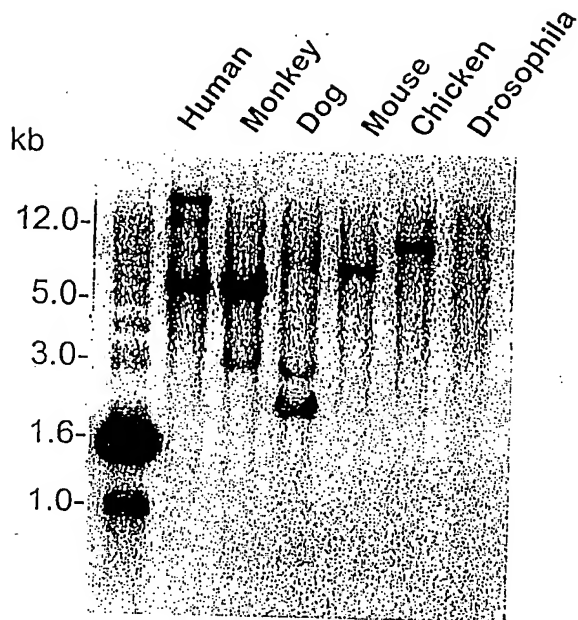
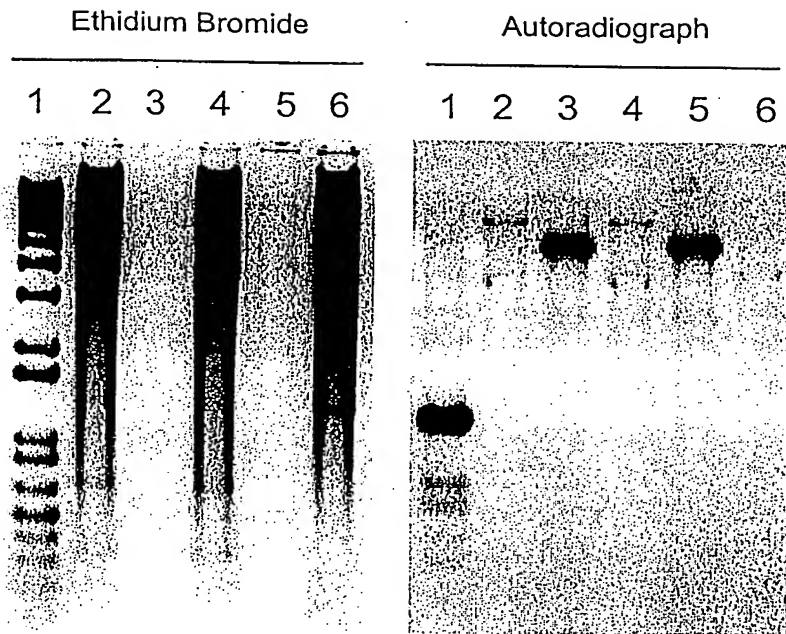


FIG. 20

**Lanes**

- 1) 1kb ladder
- 2) human female genomic
- 3) 12P11 BAC mus
- 4) human female genomic
- 5) 12P11 BAC mus
- 6) 3T3